Supplementary Materials

Comprehensive assessment showed no association of variants at the *SLC10A1* locus with susceptibility to persistent HBV infection among Southern Chinese

Short title: *SLC10A1* variants and persistent HBV infection

Ying Zhang[1,2,6,7,*], Yuanfeng Li[2,6,7,*], Miantao Wu[9,*], Pengbo Cao[2,6,7], Xiaomin Liu[10], Qian Ren[2,6,7], Yun Zhai[2,6,7], Bobo Xie[2,6,7], Yanling Hu[3], Zhibin Hu[4], Jinxin Bei[5], Jie Ping[2,6,7], Xinyi Liu[2,6,7], Yinghua Yu[8], Bingqian Guo[2,6,7], Hui Lu[2,6,7], Guanjun Liu[8], Haitao Zhang[2,6,7], Ying Cui[8], Zengnan Mo[3], Hongbing Shen[4],Yi-Xin Zeng[5], Fuchu He[1,2,6,7], Hongxing Zhang[2,6,7], and Gangqiao Zhou[2,6,7]

[1]School of Life Sciences, Tsinghua University, Beijing, China;

[2] State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, Beijing, China;

[3]Center for Genomic and Personalized Medicine, Guangxi Medical University, Nanning, Guangxi, China;

[4]Department of Epidemiology and Biostatistics, MOE Key Laboratory of Modern Toxicology, School of Public Health, Nanjing Medical University, Nanjing, China;

[5]State Key Laboratory of Oncology in Southern China, Guangzhou, China;

[6]National Engineering Research Center for Protein Drugs, Beijing, China;

[7]National Center for Protein Sciences Beijing, Beijing, China;

[8]Affiliated Cancer Hospital of Guangxi Medical University, Nanning, Guangxi, China;

[9] State Key Laboratory of Oncology in South China, Collaborative Innovation Center for Cancer Medicine, Sun Yat-sen University Cancer Center, Guangzhou, China;

[10] Department of Laboratory Medicine, Sun Yat-sen University Cancer Center, Guangzhou, China.

*These authors contributed equally to this work.

Correspondence should be addressed to:

Dr. Gangqiao Zhou, State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, 27 Taiping Road, Beijing 100850, P. R. China. E-mail: zhougq114@126.com; Phone: 86-10-66931204.

or

Dr. Hongxing Zhang, State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, 27 Taiping Road, Beijing 100850, P. R. China. E-mail: zhanghx08@126.com; Phone &fax: 86-10-61777099.

or

Dr. Fuchu He, State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, 27 Taiping Road, Beijing 100850, P. R. China. E-mail: hefc@nic.bmi.ac.cn; Phone &fax: 86-10-68177417.

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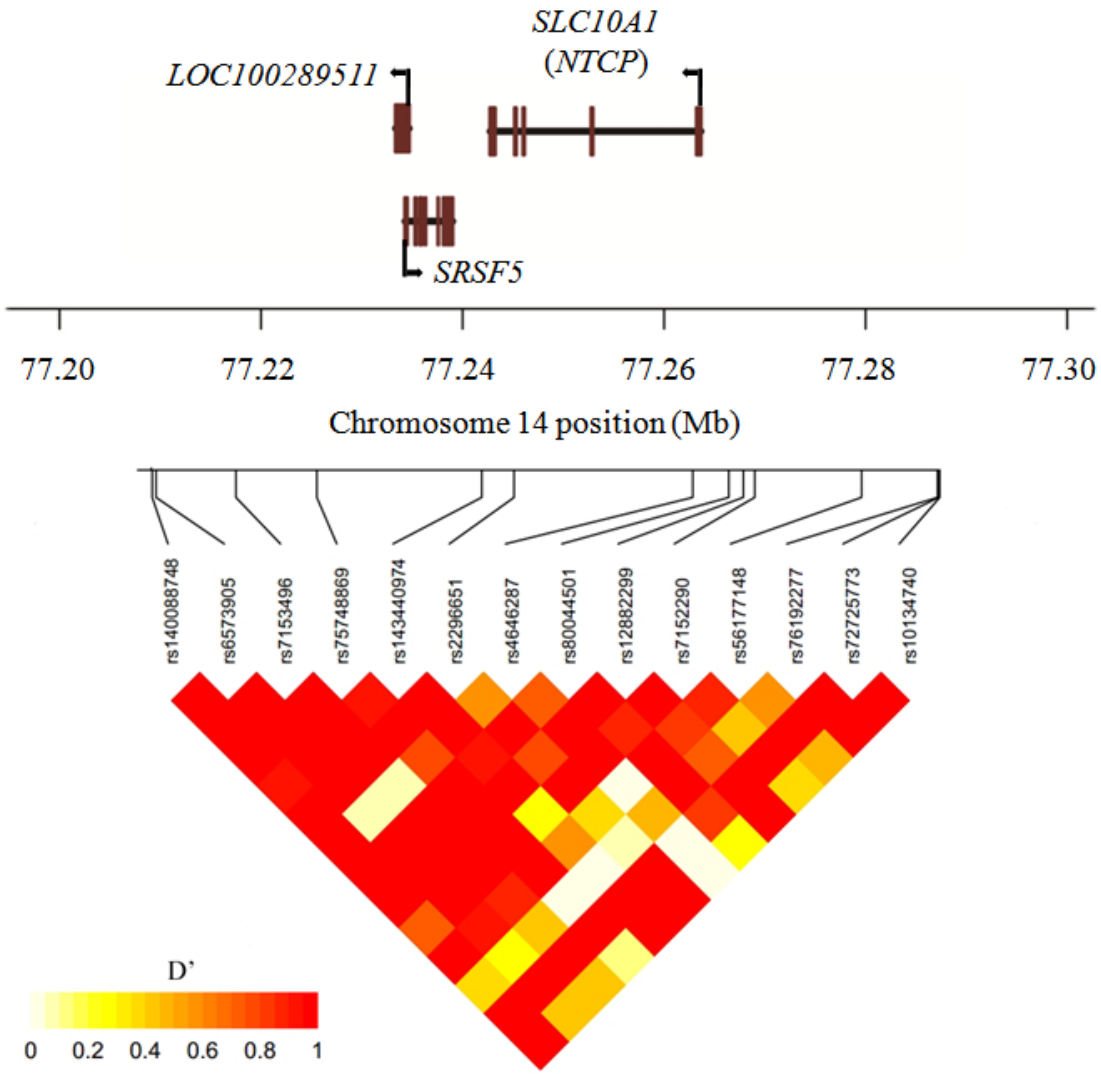
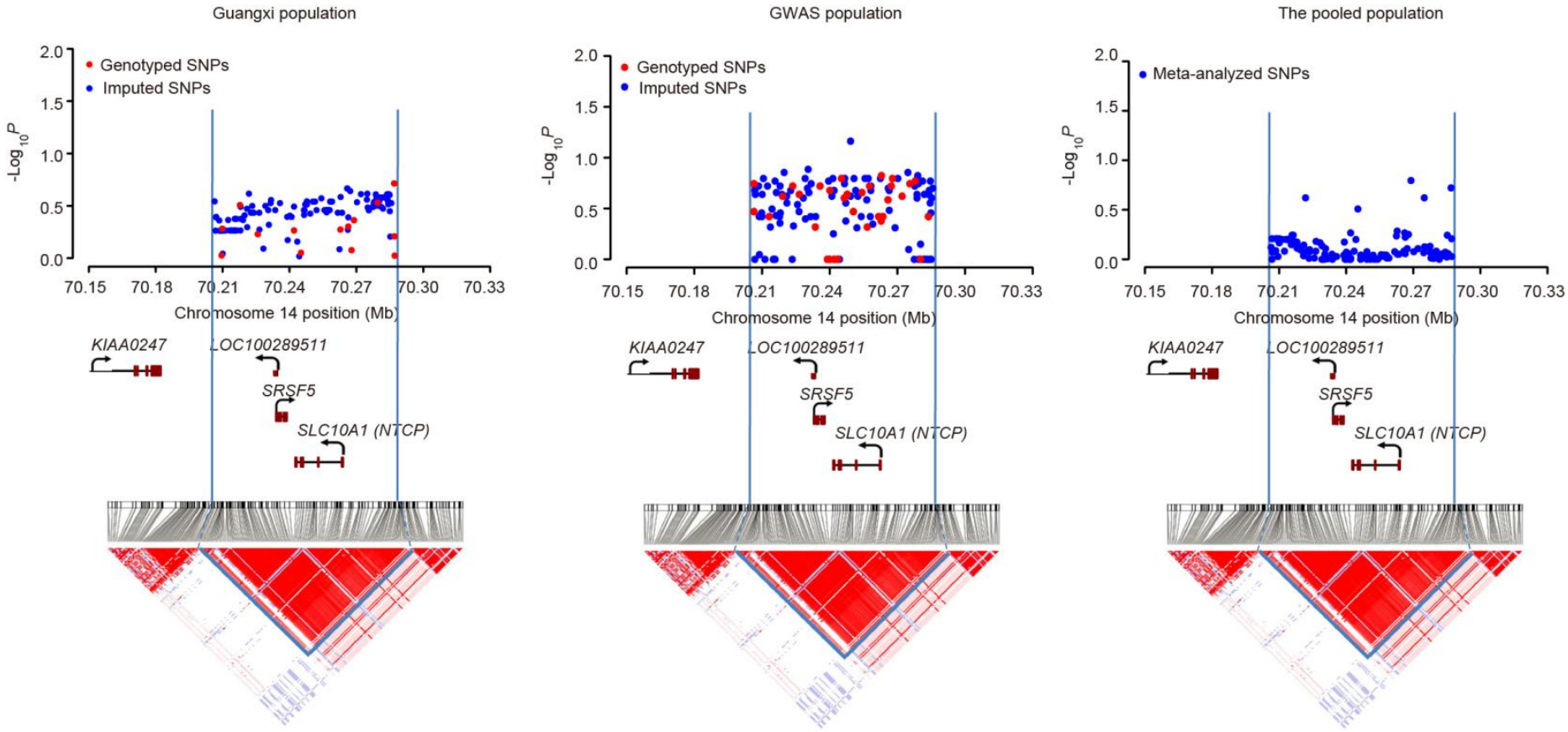
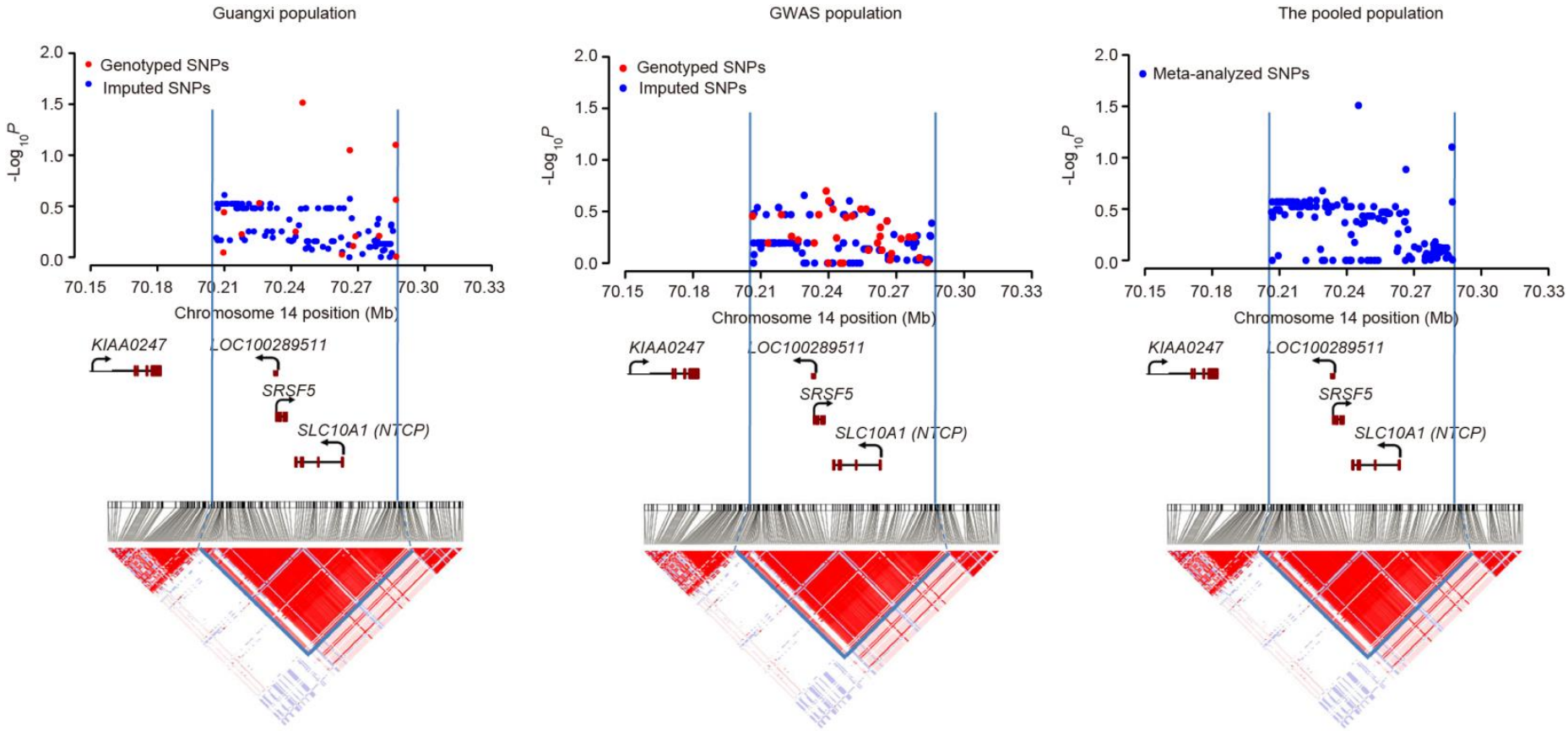


Supplementary Figure 1: Fourteen haplotype-tagging SNPs (htSNPs) in the *SLC10A1* region. Genomic locations of genes on the NCBI Build 37 human assembly were adapted from the University of California at Santa Cruz Genome Browser (http://genome.ucsc.edu/). The LD structure surrounding the *SLC10A1* gene in Chinese CHB and CHS samples of the 1000 Genomes Project was shown. Shading represents the magnitude and significance of pairwise LD (measured by *D'*), with a red-to-white gradient reflecting higher to lower LD values.

A.


Guangxi population
GWAS population
The pooled population
Genotyped SNPs
Imputed SNPs
Meta-analyzed SNPs
-Log10P
2.0
1.5
1.0
0.5
0.0
70.15
70.18
70.21
70.24
70.27
70.30
70.33
Chromosome 14 position (Mb)
KIAA0247
LOC100289511
SRSF5
SLC10A1 (NTCP)

B.


Guangxi population
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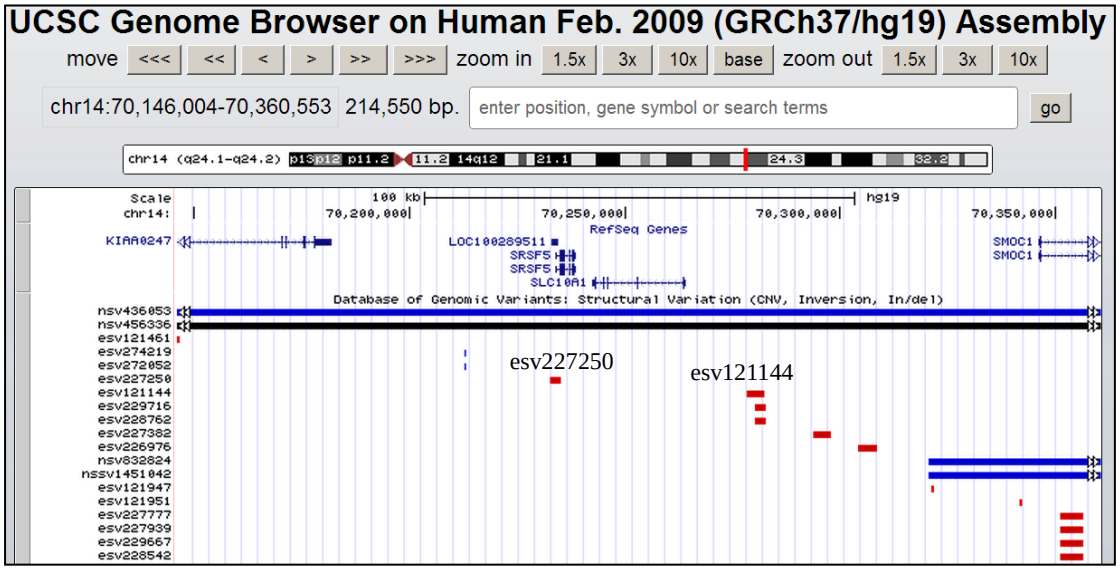
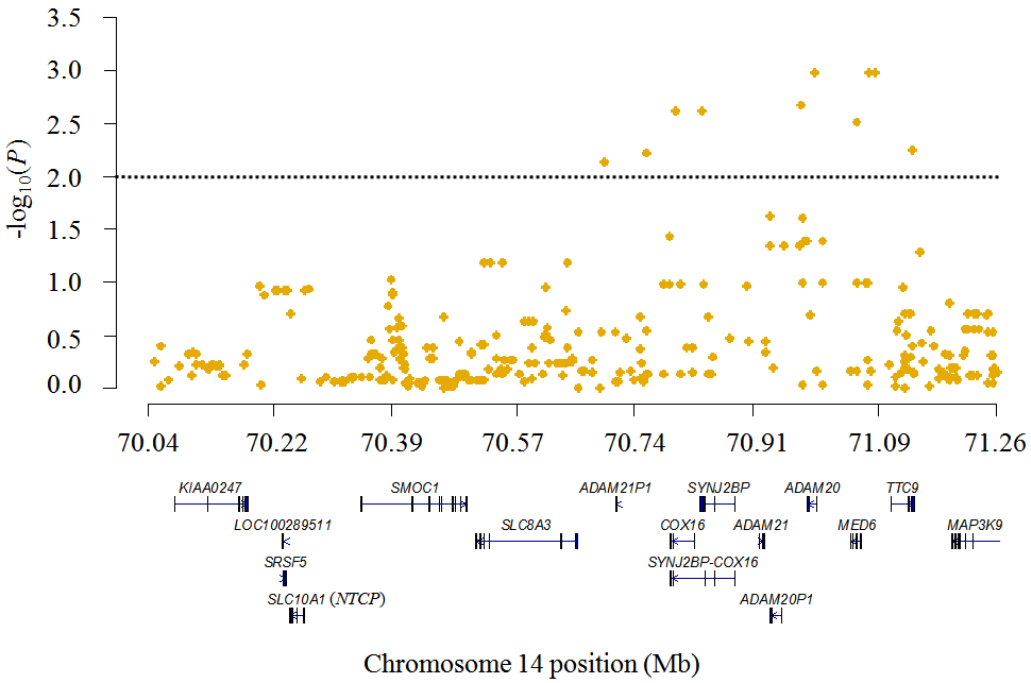
Supplementary Figure 2: The association results of genotyped and imputed SNPs in the Sample Set 1 (Guangxi population), the Sample Set 2 (GWAS population), and the pooled population. SNPs surrounding *SLC10A1* are plotted with their *P* values (shown as $-\log_{10}$ values) for dominant (A), and recessive (B) model tests as a function of genomic position (NCBI Build 37) in the Sample Set 1, the Sample Set 2, and the pooled population by meta-analyses. Genomic locations of genes on the NCBI Build 37 human assembly were adapted from the University of California at Santa Cruz Genome Browser (http://genome.ucsc.edu/). The LD structure surrounding the *SLC10A1* gene in Chinese CHB and CHS samples of the 1000 Genomes Project was shown. Shading represents the magnitude and significance of pairwise LD (measured by *D'*), with a red-to-white gradient reflecting higher to lower LD values. The most intense red spots have a *D'*= 1.

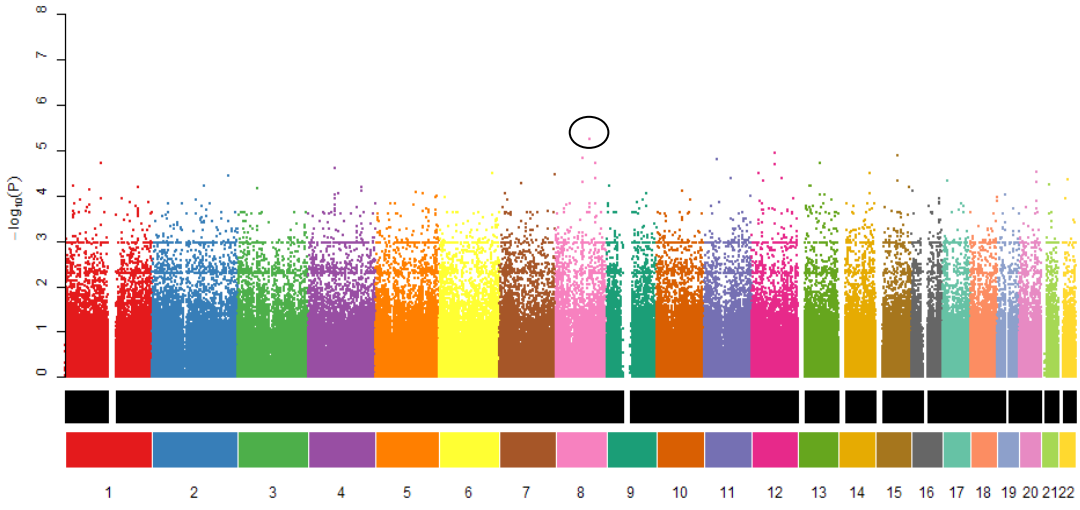


Supplementary Figure 3: The known CNVs covering *SLC10A1* and its flanking region. The nearest CNVs flanking *SLC10A1* documented in the database of genomic variants (DGV) were two deletions, of which one (esv227250, chr14:70232648-70235147, 2.5-Kb in length) located 7.4-Kb downstream and the other (esv121144, chr14:70278335-70282507, 4.2-Kb in length) 14.3-Kb upstream of *SLC10A1*. The figure was adapted from the University of California at Santa Cruz Genome Browser (http://genome.ucsc.edu/).

A.

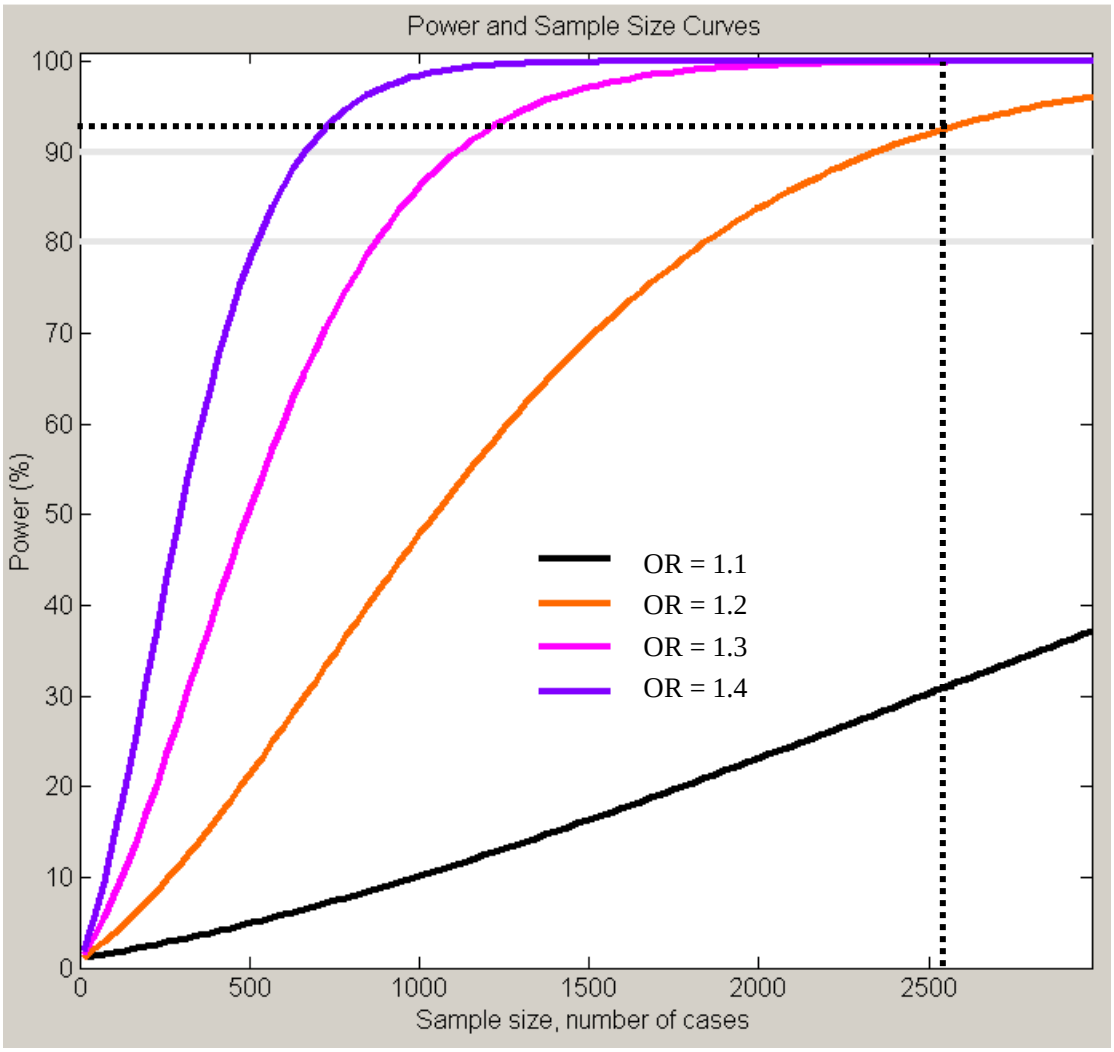


B.



Supplementary Figure 4: Graphical scheme of eQTL obtained by ANOVA analysis in the liver tissues of 31 persistent HBV infected subjects (PIs). A, Cis-eQTL analysis indicated that no SNPs within the 1-Mb upstream and 200-kb downstream of *SLC10A1* showed significant association (P<0.001) with *SLC10A1* expression, with

10 SNPs showing marginally significance (P<0.01). B, Trans-eQTL analysis indicated that no genome-wide significant trans-eSNPs ($P<5.0\times10^{-8}$) were found, with only two SNPs rs3133759 and rs13255741 (the circled points) showing nominal significance ($P= 5.8\times10^{-6}$). The x-axis represents genomic position (NCBI Build 37), and the y-axis shows $-\log_{10}(P)$. Within each chromosome shown on the x-axis, the data are plotted from the p-ter end.



Supplementary Figure 5: Power to detect a genetic effect of various sizes (OR = 1.1, 1.2, 1.3, or 1.4) versus study sample size. Power is reported here as the probability of SNPs to be identified in a scan. Vertical and horizontal dashed lines show that the power of our pooled population (totally 2,550 cases and 2,124 controls), at significance level of 0.01, to detect an allele with a minor allele frequency (MAF) of 0.20 that confers an additive 1.2-fold effect on risk of persistent HBV infection, was estimated to be ~92%.